domain, amino acids conserved in vertebrate TSP type-1rpeats are shown by a plus (+). The mutation, *gon-1(q518),* is marked by an inverted triangle (V). For the TSPt1-like repeats, only 2 of the 17 are shown. The consensus sequence for these repeats is: W-X_{4-5}-W-X_2-CS-X_2-CG-X_{4-5}-X-G-X_3-R-X_3-C-X_{4-27}C-X_{8-12}-C-X_{3-4}-C (SEQ ID NO:3). Because only the first two TSPt1-like motifs are shown, the other mutations are not indicated in this figure.

In the Claims:

Please amend Claims 1 and 6-9 as follows:

1. (Twice amended) A method for identifying in a nematode having a developing gonadal cell a modulator of a gonadal cell migration activity of a protein in the nematode, wherein the protein comprises a metalloprotease domain and a thrombospondin domain, the nematode being selected from the group consisting of *C. elegans* and *C. briggsae*, the method comprising the steps of:

treating the nematode with at least one potential modulator of gonadal cell migration; and

observing in the treated nematode a change in migration or shape of the developing gonadal cell attributable to modulation of the migration activity by the at least one potential modulator, wherein a change in the migration or shape of the developing gonadal cell results in the identification of the modulator.

2. A method as claimed in Claim 1 wherein migration of the developing gonadal cell in the nematode before treatment is absent or reduced relative to a wild type individual.

3. A method as claimed in Claim 1 wherein the treating step restores or enhances migration in the nematode relative to migration before the treating step.

4. A method as claimed in Claim 1 wherein migration of the developing gonadal cell in the nematode before treatment is at a level of a wild type individual.

5. A method as claimed in Claim 1 wherein the treating step reduces migration in the nematode relative to migration before the treating step.

6. (Twice Amended) A method as claimed in Claim 1, the protein being selected from the group consisting of a protein encoded by a native polynucleotide sequence, a protein

encoded by a heterologous polynucleotide sequence introduced into the nematode, a protein that shares at least 20% amino acid sequence identity in the metalloprotease and thrombospondin domains with either of the foregoing and that retains functional metalloprotease and thrombospondin domains, and a chimeric protein that retains functional metalloprotease and thrombospondin domains, the heterologous polynucleotide sequence being under transcriptional control of a promoter active in a tissue located sufficiently close to the developing gonadal cell such that the protein can direct the cell to migrate.

C3

7. (Twice amended) A method as claimed in Claim 6, wherein the native polynucleotide sequence is SEQ ID NO:1.

8. (Twice amended) A method as claimed in Claim 6, wherein the heterologous polynucleotide sequence is a homolog of SEQ ID NO:1.

9. (Amended) A method as claimed in Claim 8 wherein the homolog of SEQ ID NO:1 encodes a metalloprotease enzyme selected from the group consisting of murine ADAMTS-1 protein, bovine procollagen-1 N-proteinase, and human aggrecan-degrading metalloprotease.

10. A method as claimed in Claim 6 wherein the protein is truncated relative to a protein in a wild type individual.

13. A method as claimed in Claim 1 wherein the at least one modulator is selected from the group consisting of a nucleic acid molecule, a protein molecule, a sugar, a lipid, an organic molecule, a synthetic or natural pharmaceutical agent, and a mixture thereof.